

SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

<120> A new aminopeptidase and the gene encoding the peptidase

<130> Y1J0140

<150> JP 2001-78930

<151> 2001-03-19

<150> JP 2001-293348

<151> 2001-09-26

<160> 15

<170> PatentIn Ver. 2.1

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<211> 3383

<212> DNA

<213> *Aspergillus nidulans*

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<212> DNA

<213> Aspergillus nidulans

<220>

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<222> (72)..(1628)

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Met Ala Lys Lys Ile Leu Ser Asp Ile His His His Glu

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tct aac ttg gct tac cgc cag tat gcc cag ctg cct gaa acc ctc cac 158
Ser Asn Leu Ala Tyr Arg Gln Tyr Ala Gln Leu Pro Glu Thr Leu His
15 20 25

ctc aac tac cag cct cct act gct act gca acc ccc gcc gca cac acc 206
Leu Asn Tyr Gln Pro Pro Thr Ala Thr Ala Thr Pro Ala Ala His Thr
30 35 40 45

agc ccg atc cca gag gca atc aac ccc gac gat tac tcg cag gct tac 254
Ser Pro Ile Pro Glu Ala Ile Asn Pro Asp Asp Tyr Ser Gln Ala Tyr
50 55 60

tgc gat ttt atg act gag cat ccc acc att ttt cac gca gtc gat ggc 302
Cys Asp Phe Met Thr Glu His Pro Thr Ile Phe His Ala Val Asp Gly
65 70 75

ttc tct aag caa ctc gaa aag gga tac aag tac cta tcc gag cgg	350		
Phe Ser Lys Gln Leu Glu Ser Lys Gly Tyr Lys Tyr Leu Ser Glu Arg			
80	85	90	
gaa tta tgg acg ccg cag ctc aaa cgc gga gga aag tac tat acg act	398		
Glu Leu Trp Thr Pro Gln Leu Lys Arg Gly Gly Lys Tyr Tyr Thr Thr			
95	100	105	
cgc aat gga agc tcg ttg att gcg ttc tct gtc ggc ccc gag tat aag	446		
Arg Asn Gly Ser Ser Leu Ile Ala Phe Ser Val Gly Pro Glu Tyr Lys			
110	115	120	125
agt ggg aat ggc ctc gct atc atc gcc ggc cac att gat gcc ctc acg	494		
Ser Gly Asn Gly Leu Ala Ile Ile Ala Gly His Ile Asp Ala Leu Thr			
130	135	140	
gcg aag ctc aag ccc gtc tca aaa ctt ccc aat aaa gct gga tac att	542		
Ala Lys Leu Lys Pro Val Ser Lys Leu Pro Asn Lys Ala Gly Tyr Ile			
145	150	155	
cag atg gga gtt gct cct tat gcc ggc ggt ctg ggc aag aca tgg tgg	590		
Gln Met Gly Val Ala Pro Tyr Ala Gly Gly Leu Gly Lys Thr Trp Trp			
160	165	170	
gac cgt gat ttg tct atc ggc ggg aag gtt ctc gtt cgt aac gct agc	638		
Asp Arg Asp Leu Ser Ile Gly Gly Lys Val Leu Val Arg Asn Ala Ser			
175	180	185	
acc ggc aag gtt gaa tcc aag cta gtc aag ttg aac tgg ccg att gct	686		

Thr Gly Lys Val Glu Ser Lys Leu Val Lys Leu Asn Trp Pro Ile Ala
190 195 200 205

cgc atc cca acg cta gcc gaa cac ttt ggc gct cct tcg cag ggg cca 734
Arg Ile Pro Thr Leu Ala Glu His Phe Gly Ala Pro Ser Gln Gly Pro
210 215 220

ttc aac aag gaa aca cag atg gta cct atc att gga gtc gac aac tct 782
Phe Asn Lys Glu Thr Gln Met Val Pro Ile Ile Gly Val Asp Asn Ser
225 230 235

gat ctt ttc cag tct acc act cca gcg gca gac gag ggc atc gaa ccc 830
Asp Leu Phe Gln Ser Thr Thr Pro Ala Ala Asp Glu Gly Ile Glu Pro
240 245 250

ggc acc ttt gcc tct acg cag ccc cca aaa ctc atc aaa gtg atc tcc 878
Gly Thr Phe Ala Ser Thr Gln Pro Pro Lys Leu Ile Lys Val Ile Ser
255 260 265

aag gaa ctt gga atc aca aac tac agc agc att ctc agc tgg gag cta 926
Lys Glu Leu Gly Ile Thr Asn Tyr Ser Ser Ile Leu Ser Trp Glu Leu
270 275 280 285

gaa ctt tat gac agc cag cct gca cgt atc ggc ggt att gac aag gat 974
Glu Leu Tyr Asp Ser Gln Pro Ala Arg Ile Gly Gly Ile Asp Lys Asp
290 295 300

ttt atc ttc gcc ggc cgc atc gat gac aag ctc tgc tgc tac gcc gca 1022
Phe Ile Phe Ala Gly Arg Ile Asp Asp Lys Leu Cys Cys Tyr Ala Ala

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320	325	330	
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335	340	345	
cag ggt gcc cgc tcc aac ttc atg tct agc gtc atc gaa cgc att gca 1166 Gln Gly Ala Arg Ser Asn Phe Met Ser Ser Val Ile Glu Arg Ile Ala			
350	355	360	365
caa tcc ttt gca aca tca tat gga ccc gat ctc ctt gcc caa acc gtt 1214 Gln Ser Phe Ala Thr Ser Tyr Gly Pro Asp Leu Leu Ala Gln Thr Val			
370	375	380	
gca aag agc ttc ctt atc tct gat gtc atc cac gct gtc aat ccc 1262 Ala Lys Ser Phe Leu Ile Ser Ser Asp Val Ile His Ala Val Asn Pro			
385	390	395	
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400	405	410	
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415	420	425	

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Val Ser Tyr Gly Phe Ile Lys Arg Val Ala Glu Lys Cys Gly Ser Gln
430 435 440 445

ctg cag gtc ttt caa atc cga aat gac tcc cga agc ggc gga acc att 1454
Leu Gln Val Phe Gln Ile Arg Asn Asp Ser Arg Ser Gly Gly Thr Ile
450 455 460

ggg ccc atg acc agc tcg cgg att gga atg agg gcc att gat gtc ggt 1502
Gly Pro Met Thr Ser Ser Arg Ile Gly Met Arg Ala Ile Asp Val Gly
465 470 475

atc cca cag ttg agc atg cat agc att cgc gcc acc aca ggg agt cgc 1550
Ile Pro Gln Leu Ser Met His Ser Ile Arg Ala Thr Thr Gly Ser Arg
480 485 490

gat cct ggg ctg ggt gtc aag ctg ttt aag ggg ttc ttt gat tac ttt 1598
Asp Pro Gly Leu Gly Val Lys Leu Phe Lys Gly Phe Phe Asp Tyr Phe
495 500 505

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Glu Glu Val Asp Arg Glu Phe Ser Asp Phe
510 515

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tattaagagg cttccgtcta tttgatgc 1916

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<212> PRT

<213> Aspergillus nidulans

<400> 3

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Gln Pro Pro Thr Ala Thr Ala Ala His Thr Ser Pro Ile
35 40 45

Pro Glu Ala Ile Asn Pro Asp Asp Tyr Ser Gln Ala Tyr Cys Asp Phe
50 55 60

Met Thr Glu His Pro Thr Ile Phe His Ala Val Asp Gly Phe Ser Lys
65 70 75 80

Gln Leu Glu Ser Lys Gly Tyr Lys Tyr Leu Ser Glu Arg Glu Leu Trp

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90

95

Thr Pro Gln Leu Lys Arg Gly Gly Lys Tyr Tyr Thr Thr Arg Asn Gly

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105

110

Ser Ser Leu Ile Ala Phe Ser Val Gly Pro Glu Tyr Lys Ser Gly Asn

115

120

125

Gly Leu Ala Ile Ile Ala Gly His Ile Asp Ala Leu Thr Ala Lys Leu

130

135

140

Lys Pro Val Ser Lys Leu Pro Asn Lys Ala Gly Tyr Ile Gln Met Gly

145

150

155

160

Val Ala Pro Tyr Ala Gly Gly Leu Gly Lys Thr Trp Trp Asp Arg Asp

165

170

175

Leu Ser Ile Gly Gly Lys Val Leu Val Arg Asn Ala Ser Thr Gly Lys

180

185

190

Val Glu Ser Lys Leu Val Lys Leu Asn Trp Pro Ile Ala Arg Ile Pro

195

200

205

Thr Leu Ala Glu His Phe Gly Ala Pro Ser Gln Gly Pro Phe Asn Lys

210

215

220

Glu Thr Gln Met Val Pro Ile Ile Gly Val Asp Asn Ser Asp Leu Phe

225

230

235

240

Gln Ser Thr Thr Pro Ala Ala Asp Glu Gly Ile Glu Pro Gly Thr Phe
245 250 255

Ala Ser Thr Gln Pro Pro Lys Leu Ile Lys Val Ile Ser Lys Glu Leu
260 265 270

Gly Ile Thr Asn Tyr Ser Ser Ile Leu Ser Trp Glu Leu Glu Leu Tyr
275 280 285

Asp Ser Gln Pro Ala Arg Ile Gly Gly Ile Asp Lys Asp Phe Ile Phe
290 295 300

Ala Gly Arg Ile Asp Asp Lys Leu Cys Cys Tyr Ala Ala Gln Glu Ala
305 310 315 320

Leu Met Ala Thr Ser Asp His Thr Ser Pro Ser Ser Ile Lys Met Val
325 330 335

Gly Tyr Phe Asp Asp Glu Glu Ile Gly Ser Leu Leu Arg Gln Gly Ala
340 345 350

Arg Ser Asn Phe Met Ser Ser Val Ile Glu Arg Ile Ala Gln Ser Phe
355 360 365

Ala Thr Ser Tyr Gly Pro Asp Leu Leu Ala Gln Thr Val Ala Lys Ser
370 375 380

Phe Leu Ile Ser Ser Asp Val Ile His Ala Val Asn Pro Asn Phe Leu
385 390 395 400

Asn Val Tyr Leu Glu Asn His Ala Pro Arg Leu Asn Val Gly Val Ser
405 410 415

Val Ser Ala Asp Ser Asn Gly His Met Thr Thr Asp Ser Val Ser Tyr
420 425 430

Gly Phe Ile Lys Arg Val Ala Glu Lys Cys Gly Ser Gln Leu Gln Val
435 440 445

Phe Gln Ile Arg Asn Asp Ser Arg Ser Gly Gly Thr Ile Gly Pro Met
450 455 460

Thr Ser Ser Arg Ile Gly Met Arg Ala Ile Asp Val Gly Ile Pro Gln
465 470 475 480

Leu Ser Met His Ser Ile Arg Ala Thr Thr Gly Ser Arg Asp Pro Gly
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<211> 1679

<212> DNA

<213> Aspergillus oryzae

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Met Thr Lys Arg Ser Val Leu Asp Leu Arg Asp Ser Ala

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atg gct tat cgc ctg tcg gcc cag ctt cct gag ccc tcc cca gcc acc 159

Met Ala Tyr Arg Leu Ser Ala Gln Leu Pro Glu Pro Ser Pro Ala Thr

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20

25

att gca acc cca gtg gcg agg agt ggc ccc ttc gcc ccg gaa gat tac 207

Ile Ala Thr Pro Val Ala Arg Ser Gly Pro Phe Ala Pro Glu Asp Tyr

30

35

40

45

acg aaa cca tac tgc gaa ttc atg aca gca aac ccc aca atc ttt cac 255

Thr Lys Pro Tyr Cys Glu Phe Met Thr Ala Asn Pro Thr Ile Phe His

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60

gcc gtt gat ggt ttc acc agg cag ctc gaa agc cag gga tac aag cgc 303

Ala Val Asp Gly Phe Thr Arg Gln Leu Glu Ser Gln Gly Tyr Lys Arg

65

70

75

ctt ccc gag cgc gag acg tgg aac tcc aag tta gag aag ggt ggg aag	351	
Leu Pro Glu Arg Glu Thr Trp Asn Ser Lys Leu Glu Lys Gly Gly Lys		
80	85	90
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Tyr Tyr Val Thr Arg Asn Gly Ser Ala Phe Ile Ser Phe Ser Ile Gly		
95	100	105
aga gat tat aaa agt ggc aat gga atg gcc att gtt gca ggt cat atc	447	
Arg Asp Tyr Lys Ser Gly Asn Gly Met Ala Ile Val Ala Gly His Ile		
110	115	120
125		
gat gca ctc acc gcc aaa ttg aag ccc gtg tcc aag ctg ccc aac aag	495	
Asp Ala Leu Thr Ala Lys Leu Lys Pro Val Ser Lys Leu Pro Asn Lys		
130	135	140
gct ggc ttt tcc cag ctc gga gtt gcg ccc tac gca ggc gct ctg agt	543	
Ala Gly Phe Ser Gln Leu Gly Val Ala Pro Tyr Ala Gly Ala Leu Ser		
145	150	155
gac aca tgg tgg gac cgc gat ctc tca ata ggt ggc cgt gtt ctg gtc	591	
Asp Thr Trp Trp Asp Arg Asp Leu Ser Ile Gly Gly Arg Val Leu Val		
160	165	170
caa gac tcc aac acc ggg aaa gtc gag tcc aaa tta gtc aaa ttg gac	639	
Gln Asp Ser Asn Thr Gly Lys Val Glu Ser Lys Leu Val Lys Leu Asp		
175	180	185

tgg ccc att gct cgg atc cca acc ctg gca cct cat ttc ggg gct ccc 687
Trp Pro Ile Ala Arg Ile Pro Thr Leu Ala Pro His Phe Gly Ala Pro
190 195 200 205

tcg caa ggc ccc ttc aac aaa gag act cag atg gtg cct ata att ggc 735
Ser Gln Gly Pro Phe Asn Lys Glu Thr Gln Met Val Pro Ile Ile Gly
210 215 220

gtt gat aac tcc gat ctt ttc cag cag caa gcc cca tcc aag ata gat 783
Val Asp Asn Ser Asp Leu Phe Gln Gln Gln Ala Pro Ser Lys Ile Asp
225 230 235

caa gac aac ggg atc aaa cct ggt aca ttt gca gcc acg caa ccg gaa 831
Gln Asp Asn Gly Ile Lys Pro Gly Thr Phe Ala Ala Thr Gln Pro Glu
240 245 250

aag ctt gtc aaa gtc ata tcc aag gag ctt ggt atc aca gac tac agc 879
Lys Leu Val Lys Val Ile Ser Lys Glu Leu Gly Ile Thr Asp Tyr Ser
255 260 265

tcg att ata agc tgg gag ctg gag ctg tat gac agt caa cca gca caa 927
Ser Ile Ile Ser Trp Glu Leu Glu Leu Tyr Asp Ser Gln Pro Ala Gln
270 275 280 285

gtt ggt ggc ctg gac aag gac ctg att ttt gct ggt cgc att gac gat 975
Val Gly Gly Leu Asp Lys Asp Leu Ile Phe Ala Gly Arg Ile Asp Asp
290 295 300

aag ctc tgc tgc tat gcc gct cag gaa gct ctg ctt gcc tca tcc gac 1023

Lys Leu Cys Cys Tyr Ala Ala Gln Glu Ala Leu Leu Ala Ser Ser Asp
305 310 315

agt act tca act agc tct atc aag atg gtc ggt atg ttt gat gac gag 1071
Ser Thr Ser Thr Ser Ser Ile Lys Met Val Gly Met Phe Asp Asp Glu
320 325 330

gaa att gga agc ctg ctt cgc cag gga gct cga tcc aac ttc atg agc 1119
Glu Ile Gly Ser Leu Leu Arg Gln Gly Ala Arg Ser Asn Phe Met Ser
335 340 345

agt gtc ata gag cgt att acg gaa gcc ttc tca ccc aat tac ggt cct 1167
Ser Val Ile Glu Arg Ile Thr Glu Ala Phe Ser Pro Asn Tyr Gly Pro
350 355 360 365

aac gtg ctg tct caa act gtg gcg aac agc ttc ttc gtg tct tcg gac 1215
Asn Val Leu Ser Gln Thr Val Ala Asn Ser Phe Phe Val Ser Ser Asp
370 375 380

gtc atc cat gcg gtc aat ccg aac ttc ctt ggt gtc tat ctt gag aac 1263
Val Ile His Ala Val Asn Pro Asn Phe Leu Gly Val Tyr Leu Glu Asn
385 390 395

cat gct ccc cgt ctg aac gtc ggt gtg gcc gtc tcg gct gac tct aac 1311
His Ala Pro Arg Leu Asn Val Gly Val Ala Val Ser Ala Asp Ser Asn
400 405 410

ggc cat atg aca aca gac agt gtg agc tac gga ttc atc aag cgt gtc 1359
Gly His Met Thr Thr Asp Ser Val Ser Tyr Gly Phe Ile Lys Arg Val

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tcc cgt agt ggc ggg act att gga ccc atg acc agt tct cgc att ggc 1455			
Ser Arg Ser Gly Gly Thr Ile Gly Pro Met Thr Ser Ser Arg Ile Gly			
450	455	460	
atg agg gcc att gac gtg ggg atc ccg cag ttg agt atg cac agt atc 1503			
Met Arg Ala Ile Asp Val Gly Ile Pro Gln Leu Ser Met His Ser Ile			
465	470	475	
cgt gcg act acc ggt agt ttg gat ccg gga ttg ggt gtg aag ctg ttc 1551			
Arg Ala Thr Thr Gly Ser Leu Asp Pro Gly Leu Gly Val Lys Leu Phe			
480	485	490	
aag ggc ttt ttc gac tat ttc gag gag gtg gac aag gaa ttt gca gat 1599			
Lys Gly Phe Phe Asp Tyr Phe Glu Glu Val Asp Lys Glu Phe Ala Asp			
495	500	505	
ttc tgatgcgctc ctctgaaata ctagggaaatg tttccatcgtaa gtatcgtaa 1652			
Phe			
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<212> PRT

<213> Aspergillus oryzae

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Arg Leu Ser Ala Gln Leu Pro Glu Pro Ser Pro Ala Thr Ile Ala Thr

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30

Pro Val Ala Arg Ser Gly Pro Phe Ala Pro Glu Asp Tyr Thr Lys Pro

35

40

45

Tyr Cys Glu Phe Met Thr Ala Asn Pro Thr Ile Phe His Ala Val Asp

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60

Gly Phe Thr Arg Gln Leu Glu Ser Gln Gly Tyr Lys Arg Leu Pro Glu

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70

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80

Arg Glu Thr Trp Asn Ser Lys Leu Glu Lys Gly Gly Lys Tyr Tyr Val

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Thr Arg Asn Gly Ser Ala Phe Ile Ser Phe Ser Ile Gly Arg Asp Tyr

100

105

110

Lys Ser Gly Asn Gly Met Ala Ile Val Ala Gly His Ile Asp Ala Leu

115

120

125

Thr Ala Lys Leu Lys Pro Val Ser Lys Leu Pro Asn Lys Ala Gly Phe
130 135 140

Ser Gln Leu Gly Val Ala Pro Tyr Ala Gly Ala Leu Ser Asp Thr Trp
145 150 155 160

Trp Asp Arg Asp Leu Ser Ile Gly Gly Arg Val Leu Val Gln Asp Ser
165 170 175

Asn Thr Gly Lys Val Glu Ser Lys Leu Val Lys Leu Asp Trp Pro Ile
180 185 190

Ala Arg Ile Pro Thr Leu Ala Pro His Phe Gly Ala Pro Ser Gln Gly
195 200 205

Pro Phe Asn Lys Glu Thr Gln Met Val Pro Ile Ile Gly Val Asp Asn
210 215 220

Ser Asp Leu Phe Gln Gln Gln Ala Pro Ser Lys Ile Asp Gln Asp Asn
225 230 235 240

Gly Ile Lys Pro Gly Thr Phe Ala Ala Thr Gln Pro Glu Lys Leu Val
245 250 255

Lys Val Ile Ser Lys Glu Leu Gly Ile Thr Asp Tyr Ser Ser Ile Ile
260 265 270

Ser Trp Glu Leu Glu Leu Tyr Asp Ser Gln Pro Ala Gln Val Gly Gly

275	280	285
Leu Asp Lys Asp Leu Ile Phe Ala Gly Arg Ile Asp Asp Lys Leu Cys		
290	295	300
Cys Tyr Ala Ala Gln Glu Ala Leu Leu Ala Ser Ser Asp Ser Thr Ser		
305	310	315
		320
Thr Ser Ser Ile Lys Met Val Gly Met Phe Asp Asp Glu Glu Ile Gly		
325	330	335
Ser Leu Leu Arg Gln Gly Ala Arg Ser Asn Phe Met Ser Ser Val Ile		
340	345	350
Glu Arg Ile Thr Glu Ala Phe Ser Pro Asn Tyr Gly Pro Asn Val Leu		
355	360	365
Ser Gln Thr Val Ala Asn Ser Phe Phe Val Ser Ser Asp Val Ile His		
370	375	380
Ala Val Asn Pro Asn Phe Leu Gly Val Tyr Leu Glu Asn His Ala Pro		
385	390	395
		400
Arg Leu Asn Val Gly Val Ala Val Ser Ala Asp Ser Asn Gly His Met		
405	410	415
Thr Thr Asp Ser Val Ser Tyr Gly Phe Ile Lys Arg Val Ala Asp Arg		
420	425	430

Cys Gly Ser Thr Leu Gln Val Phe Gln Ile Arg Asn Asp Ser Arg Ser
435 440 445

Gly Gly Thr Ile Gly Pro Met Thr Ser Ser Arg Ile Gly Met Arg Ala
450 455 460

Ile Asp Val Gly Ile Pro Gln Leu Ser Met His Ser Ile Arg Ala Thr
465 470 475 480

Thr Gly Ser Leu Asp Pro Gly Leu Gly Val Lys Leu Phe Lys Gly Phe
485 490 495

Phe Asp Tyr Phe Glu Glu Val Asp Lys Glu Phe Ala Asp Phe
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